



Single Nucleotide Polymorphism



PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy
Search	SNP	▼	for			
Limits Preview/Index History Clipboard Details						

dbSNP BUILD 110

Reference SNP Cluster Report

GENERAL

dbSNP Home Page
 SNP Science Primer
 Announcements
 dbSNP Summary
 FTP SERVER

Getting Started **NEW**
 Build History
 Handle Request

DOCUMENTATION

FAQ
 Overview
 How To Submit
 RefSNP Summary Info
 Database Schema
 html
 pdf
 Data formats
 Heterozygosity
 computation

SEARCH

Entrez SNP **NEW**
 Blast SNP
 Batch query
 By Submitter
 New Batches
 Method
 Population
 Detail
 Class
 Publication
 Chromosome Report
 Locus Information
 STS Markers
 Free Form Search
 Simple
 Advance

HAPLOTYPE

Specifications
 Sample HapSet
 Sample Individual

NCBI SNP CLUSTER ID:

rs5962

Organism:

human (*Homo sapiens*)

Variation Class:

SNP: single nucleotide polymorphism

Molecule Type:

Genomic

dbSNP build of first appearance:

52 9/99

dbSNP build of most recent change to cluster:

52

Current dbSNP build:

110

SNP Details are categorized in the following sections:

Submission	Fasta	Resource	Locus	Map	Variation
------------	-------	----------	-------	-----	-----------

Submitter records for this RefSNP Cluster

The submission **ss7572** has the longest flanking sequence of all cluster members BLAST analysis for the current build.

NCBI Assay ID	Handle/Submitter ID	Validation Status	Entry Date	Update Date	Build Added
---------------------	---------------------	----------------------	---------------	----------------	----------------

ss7572 WIAF-CSNP|WIAF-11044



07/15/99 01/29/01 52

Fasta sequence (Legend)

>gnl|dbSNP|rs5962|allelePos=101|totalLen=201|taxid=9606|snpclass=1|alleles=''

TGGCACCCTT GGGCCAGCCC AGCCTCCATT TCTCCAGCTG TCCCCAGAGC CAACGTGC
 CTCCTTTGGC AGTCACACGG AAGCTCTGCA GCCTGGACAA
 Y
 GGGGACTGTG ACCAGTTCTG CCACGAGGAA CAGAACTCTG TGGTGTGCTC CTGCGCCC
 GGGGACTGTG ACCAGTTCTG CCACGAGGAA CAGAACTCTG TGGTGTGCTC CTGCGCCC

GGGTACACCC TGGCTGACAA CGGCAAGGCC TGCATTCCCA

NCBI Resource Links**Submitter-Referenced Accessions:**GenBank: [L00394](#)**dbSNP Blast Analysis:**GenBank HTGS Finished: [AB005892.1](#) [AF503510.1](#) [AL137002.1](#)**LocusLink Analysis**LocusLink via analysis of contig annotation: [F10](#) coagulation factor X

Gene Model (contig mRNA transcript) information from genome sequence for



Contig accession	Contig position	Protein accession	Function	dbSNP allele	Protein residue	Cod posi
NT_027140	1291267	NP_000495	contig reference	C	Asn [N]	3
			synonymous change	T	Asn [N]	3

LocusLink via BLAST analysis of mRNAs: [F10](#) coagulation factor X

Variations are assigned to a gene if mapped within 2 kb of mRNA sequence feature.

Accession class	Nucleotide accession	Nucleotide Position	Hit orientation	Protein accession	Function
HTGS finished	AB005892.1	105	plus strand	BAA21634.1	locus

Integrated Maps:NCBI MapViewer: [rs5962](#) maps exactly once on NCBI human [chromosome 1](#).

Chromosome	Contig accession	Contig Position	Chromosome Position	Hit orientation
13	NT_027140.5	1291267	108432435	plus strand

NCBI Sequence Viewer: See [rs5962](#) in Sequence Viewer.Project Ensembl: Query [rs5962](#) in Ensembl.

UC Santa Cruz Genome Assembly: Query [rs5962](#) on the Santa Cruz Assembly**Variation Summary:**

Assay sample size (number of chromosomes): 114
Population data sample size (number of chromosomes): 106
Total number of populations with frequency data: 1
Total number of individuals with genotype data: 0
Average estimated heterozygosity: 0.047
Average Allele Frequency:
C 0.972
T 0.028

Validation Summary:

Marker displays Mendelian segregation: UNKNOWN
PCR results confirmed in multiple reactions: YES
Homozygotes detected in individual genotype data: UNKNOWN

Validation status:

GENERAL: [Home Page](#) | [Announcements](#) | [dbSNP Summary](#) | [Genome](#) | [FTP SERVER](#) | [Build H](#)
DOCUMENTATION: [FAQ](#) | [Overview](#) | [How To Submit](#) | [RefSNP Summary Info](#) | [Database Sc](#)
SEARCH: [Entrez SNP](#) | [Blast SNP](#) | [Main Search](#) | [Batch query](#) | [By Submitter](#) | [New Batches](#) | [Me](#)
| [Chromosome Report](#) | [Batch](#) | [Locus Info](#) | [Freeform](#) | [EasyForm](#) | [Between Marker](#)
HAPLOTYPE: [Specifications](#) | [Sample HapSet](#) | [Sample Individual](#)
NCBI: [PubMed](#) | [Entrez](#) | [BLAST](#) | [OMIM](#) | [Taxonomy](#) | [Structure](#)

[Disclaimer](#) [Privacy statement](#)

Revised December 12, 2002 9:18 AM